

RA TUSHINSKI R.J., MOCHIZUKI D.Y., LARSEN A., GRABSTEIN K., COSMAN D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:6250-6254 (1985).
 RN [4]

RP SEQUENCE FROM N.A.

RM 85218749

RA WONG G.G., WITEK J.S., TEMPLE P.A., WILKENS K.M., LEARY A.C.,
 RA LUXENBERG D.P., JONES S.S., BROWN E.L., KAY R.M., ORR E.C.,
 RA SHOMAKER C., GOLDE D.W., KAUFMAN R.J., HEWICK R.M., WANG E.A.,
 RA CLARK S.C.;
 RL SCIENCE 228:810-815 (1985).
 RN [5]

RP SEQUENCE FROM N.A.

RM 86030234

RA MIYATAKE S., OTSUKA T., YOKOTA T., LEE F., ARAI K.-I.;
 RL EMBO J. 4:2561-2568 (1985).
 RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).

RM 97108420

RA DIENERICH K., BOONE T., KARPLUS P.A.;
 RL SCIENCE 254:1779-1782 (1991).
 RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

RM 92235844

RA WALTER M.R., COOK W.J., EALICK S.E., NAGABHUSHAN T.L., TROTTER P.P.,
 RA BUGG C.E.;
 RL J. MOL. BIOL. 224:1075-1085 (1992).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF
 CC HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
 CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMER.

DR EMBL; M13207; HSCSFGMA.

DR EMBL; M11734; HSCSFGMB.

DR EMBL; M1220; HSCMGSPA.

DR EMBL; X03021; HSCMGSEF.

DR EMBL; M10663; HSCSFGM.

DR PIR; A01853; FQUGM.

DR PIR; C24636; C24636.

DR PIR; A25169; A25169.

DR PDB; 1CSG; 31-JAN-94.

DR PDB; 1GME; 31-OCT-93.

DR MIM; 138960; 11TH EDITION.

DR PROSITE; PS00702; GM CSF.

KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE;

KW POLYMORPHISM.

FT SIGNAL 1 17

FT CHAIN 18 144

FT GRANULOCYTE-MACROPHAGE COLONY-STIMULATING

FT FACTOR.

FT DISULFID 71 113

FT DISULFID 105 138

FT CARBOHYD 44 44

FT CARBOHYD 54 54

FT VARIANT 117 117

FT TURN 25 27

FT HELIX 30 44

FT TURN 45 45

FT HELIX 50 54

FT STRAND 56 60

FT HELIX 72 81

FT TURN 82 82

FT HELIX 85 103

I -> T.

FT TURN 104 104

FT STRAND 115 119

FT HELIX 120 131

FT TURN 132 133

SQ SEQUENCE 144 AA; 16295 MW; 112632 CN;

Query Match 99.4%; Score 1002; DB 2; Length 144;
 Best Local Similarity 95.1%; Pred. No. 4.08e-194;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslillgtvacsisaparspsstqpwehvnaigearrlnlslrdaaemnetvevi 60

Qy 1 mwlgslillgtvacsisaparspsstqpwehvnaigearrlnlslrdaaemnetvev 60

Db 61 semfdlqptclqtrilelykqglqsltklqpltmmaashyqhccpptsatqitf 120

Qy 61 semfdlqptclqtrilelykqglqsltklqpltmmaashyqhccpptsatqitf 120

Db 121 esfkenkdfllvipfdwepvq 143

Qy 121 esfkenkdfllvipfdwepvq 143

RESULT 2

ID CSF2 SHEEP STANDARD; PRT; 144 AA.

AC P28773;

DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF)

DE (COLONY-STIMULATING FACTOR) (CSF).

OS OVIS ARIES (SHEEP).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; ARTIODACTYLA.

RN [1]

RP SEQUENCE FROM N.A.

RM 92039044

RA MCINNES C.J., HAIG M.C.K.;

RL GENE 105:275-279 (1991).

CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE

CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,

CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS

CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.

CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF

CC HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING

CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.

CC -!- SUBUNIT: MONOMER.

DR EMBL; X53561; OOGMCSFR.

DR PIR; JH0469; JH0469.

DR HSSE; P04141; 1CSG.

DR PROSITE; PS00702; GM CSF.

KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 17

FT CHAIN 18 144

FT GRANULOCYTE-MACROPHAGE COLONY-STIMULATING

FT FACTOR.

FT DISULFID 71 113

FT DISULFID 105 138

FT CARBOHYD 44 44

FT POTENTIAL.

SQ SEQUENCE 144 AA; 16318 MW; 117795 CN;

Query Match 82.1%; Score 828; DB 2; Length 144;

Best Local Similarity 77.6%; Pred. No. 1.21e-154;

Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

RA	ALTJANN S.W., JOHNSON G.D., PRYSTOWSKY M.B.; J.
RJ	J. BIOL. CHEM. 266:5333-5341(1991).
RL	-I- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC	DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD. THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
CC	-I- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
CC	GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
CC	-I- SUBUNIT: MONOMER.
DR	EMB1; X03020; MGMCSPG-
DR	EMB1; X03019; MGMCSEF.
DR	EMB1; M11848; MMCSFGMC.
DR	EMB1; X02333; MGMGSEFR.
DR	EMB1; X05906; MMGCSCFL.
DR	PIR; A01854; FOMSGM.
DR	PIR; A24644; A2464A.
DR	PIR; A24645; A24645.
DR	PIR; A24636; A24636.
DR	HSSP; P04141; ICSG.
KD	PROSITE; PS00702; GM CSF.
FM	CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
FT	SIGNAL
FT	CHAIN
FT	DISULEID
FT	DISULEID
FT	CARBOHYD
FT	CARBOHYD
FT	MUTAGEN
FT	MUTAGEN
FT	MUTAGEN
FT	CONFLICT
FT	CONFLICT
FT	CONFLICT
FT	CONFLICT
SEQ	SEQUENCE
Query Match	Best Local Similarity 52.4%; Score 536; DB 2; Length 141;
Matches	Conservative 75; Conservative 20; Mismatches 45; Indels 3; Gaps 1
Db	I mnlgnllffgivyvsleaprtspilvtpkhhvealkealnld--dhpytlneevrv 57 :: : :: : : :
Gy	I mwlsqllllygtacsisapxrpsspsksxmehnalgaerrlllnlrdaeaenwexv 60 msql lgtyacsisapxrpsspsksxmehnalgaerrlllnlrdaeaenwexv 60
Db	58 snefsfkltevcqrklkfegqlrgnftklkgalmntasygytvyccptpcetdeetyvt 117 : : : : : : : : : : : : : : : : 61 semfdlepctcrlcrclrykyglgsrktlkpgllmmashyxhqcpptcpscatcqxlrf 120 semfdlepctcrlcrclrykyglgsrktlkpgllmmashyxhqcpptcpscatcqxlrf 120
Gy	118 adfidsiktfeldlpfcckppg 140 : : : : : : : : : : : : : 121 esfxenkdfllvxpfawepvg 143 esfxenkdfllvxpfawepvg 143
RESULT	5 STANDARD; PART; 605 AA.
ID	BRIE EBV
AC	P03309;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE	TRANSCRIPTION ACTIVATOR BRLE1.

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CN BRFL1.
OS EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4) .
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
RN (1)
RP SEQUENCE FROM N.A.
RM 84270667
RA BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,
RA GIBSON T.J., HATFIELD G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,
RA TOFFNELT P.S., BARRELL B.G.;
RL NATURE 310:207-211(1984) .
CC -1- FUNCTION: TRANSCRIPTION ACTIVATION.
CC -1- BRFL1 PROTEIN IS AN EARLY OR IMMEDIATE EARLY PROTEIN.
CC -1- SIMILARITY: TO HSV-1 EDRL1 (GENE 50) .
DR EMBL; V01555; EBY.
DR PIR; A03771; Q0BE29.
DR PIR; S33019; S33019.
DR TRANSFAC; T00710; -.
KM TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; EARLY PROTEIN.
SQ SEQUENCE 605 AA; 66594 MW; 1877894 CN;

Dd 483 tpaaypgpldpapavtpeasllledqdeetsqgavkaltemadvjipqkeaaaloggmdls 542
Dy 22 spspsakpnehmai-qearrll-nlstdaaenxetvrxsamlqepcdlttely 79
Dd 543 hpprghldelttllsemtednldspitpe 573
Dy 80 kqqlqselklkqplttmaashykhqcpptpe 110

RESULT 6
ID MAXS YEAST STANDARD; PRT; 581 AA.
AC P40884;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE PROBABLE ALPHA-GLUCOSIDASE HRE581 (EC 3.2.1.20) (MALTASE).
CN HRE581.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST) .
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCOMYCETES.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RA VANDENBOL M., DURAND P., BOLLE P.-A., DION C., PORTELLE D.,
RA HILGER F.;
RL YEAST 10:1657-1662(1994) .
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
CC 1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
DR EMBL; Z34098; SCATLEL.
DR PIR; S45157; S45157.
KM HYPOTHEICAL PROTEIN; HYDROLASE; GLUCOSIDASE; MALTOSE METABOLISM;
KM MULTIGENE FAMILY.
SQ SEQUENCE 581 AA; 67557 MW; 1753845 CN;

Dd 290 gelmm-fnfk-htsvgnpkcyvlpfklkfklaesfflentdcwstl 341
Dy 17 Matches 17; Conservative 9; Mismatches 23; Indels 5; Gaps 4;

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RP	SEQUENCE FROM N.A.
RH	83298546
RA	MCLEAN J.M., FUKAZAWA C., TAYLOR J.M.;
RL	J., BIOL. CHEM. 258:8933-9000(1983).
CC	-I- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON REMNANT) OF HEPATIC TISSUES.
CC	-I- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC	-I- THE MATURE PROTEIN HAS NO CYSTEINE RESIDUES; HOWEVER, IN DIFFERENT ALLELIC VARIANTS WHERE CYSTEINE RESIDUES REPLACE ARGinine AT POSITIONS 155 OR 168, BINDING OF APO-E TO CELL MEMBRANE RECEPTORS IS DECREASED. THE AMINO END OF THIS PROTEIN IS THEREFORE THOUGHT TO INTERACT WITH THE RECEPTOR.
DR	EMBL; X04979; RNAPOEC.
-DR	EMBL; J02582; RNAPOE4.
DR	PIR; A03094; LPRTF.
DR	PIR; A25576; A25576.
DR	PIR; A26189; A26189.
DR	HSPB; P02649; IIE4.
KW	GLYCOPROTEIN; PLASMA; LIPID TRANSPORT; HDL; VLDL; CHYLOMICRON;
KW	SIALIC ACID; HEPRIN-BINDING; REPEAT; SIGNAL.
FT	SIGNAL 1 18
FT	CHAIN 19 311
FT	DOMAIN 154 157
FT	DOMAIN 220 227
FT	DOMAIN 72 246
FT	REPEAT 72 93
FT	REPEAT 94 115
FT	REPEAT 116 137
FT	REPEAT 138 159
FT	REPEAT 160 181
FT	REPEAT 182 203
FT	REPEAT 204 224
FT	REPEAT 225 246
FT	CONFLICT 104 104
FT	CONFLICT 110 110
FT	CONFLICT 141 141
FT	CONFLICT 308 309
FT	CONFLICT 206 212
SO	SEQUENCE 311 AA; 36038 MW; 149056 CN;
Query Match	8.8%; Score 89; DB 1; Length 311;
Best Local Similarity	30.4%; Pred. No. 1.04e+00;
Matches 28; Conservative	19; Mismatches 37; Indels 8; Gaps 8;
Db	4 [wall]p[llt]c[a]e[e]lvtcdq[p]sgsdg[meg]dqlnrfw[d]ylrw[c]ls-dqvgeaq 62 : : : : : : : : : : : : : : Qy 1 mvlgsll-ll-gtva-csisaprxpspxqgnvh-vaiqe-arillnlstrdaaeen 55
Db	63 ssqrqtgelvlnmed-m-tevakaykkelgeel 92 : : : : : : : : : : : : : : : Qy 56 twvxsemfdlpeplclqtltlelyvkqglqsrl 87
RESULT 10	
ID AKIH_ECOLI	STANDARD; PRT; 820 AA.
AC P00561;	
DT 21-JUL-1986 (REL. 01, CREATED)	
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	
DE ASPARTOKINASE I (EC 2.7.2.4) / HOMOSERINE DEHYDROGENASE I (EC 1.1.1.3).	
EN THR4 (THR41, THR42).	

OS	ESCHERICHIA COLI.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC	ENTEROBACTERIACEAE.
OC	(1)
RP	SEQUENCE FROM N.A.
RM	81077247
RA	KATINNA M., COSSART P., STIBILLI L., SAINT-GIROUS I., CHALVIGNAC M.A.,
RA	LE BRAS G., COHEN G.N., YANIV M.,
RL	PROC. NATL. ACAD. SCI. U.S.A. 77:5730-5733(1980).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RM	9233497
RA	YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,
RA	ISONO K., MIZOBUCHI K., NAKATA A.,
RL	NUCLEIC ACIDS RES. 20:3305-3308(1992).
RL	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12 / MG1655;
RA	BURLAND V.D., PLUNKETT G. III, BLATTNER F.R.,
RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RL	[4]
RP	SEQUENCE OF 51-129.
RM	80043179
RA	STIBILLI L., LE BRAS G., COSSART P., CHALVIGNAC M.A., LE BRAS G.,
RA	BRILEY P.A., COHEN G.N.,
RL	BIOCHIMIE 61:733-739(1979).
RL	[5]
RP	REVISION TO 11.
RM	83135751
RA	COSSART P.,
RL	UNPUBLISHED RESULTS, CITED BY:
RL	ZAKIN M.M., DUCHANCE N., FERRARA P., COHEN G.N.,
RL	J. BIOL. CHEM. 258:3028-3031(1983).
CC	-I- PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON
CC	BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS,
CC	TO MET, AND TO THR AND ILE.
CC	-I- CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P) (+) = L-ASPARTATE
CC	BETA-SEMIALDEHYDE + NAD(P) H.
CC	-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
CC	ASPARTATE.
CC	-I- SUBUNIT: HOMOTETRAMER.
CC	-I- ENZYME REGULATION: THE ENZYME ACTIVITIES ARE REGULATED
CC	ALLOSTERICALLY BY L-THREONINE.
CC	-I- ASPARTOKINASE II-HOMOSERINE DEHYDROGENASE II AND ASPARTOKINASE
CC	III ALSO CATALYZE THE SAME REACTION(S).
CC	-I- SIMILARITY: TO OTHER ASPARTOKINASES AND HOMOSERINE DEHYDROGENASES
DR	EMBL; V00361; ECTHA.
DR	EMBL; J01706; ECTHR.
DR	EMBL; X68872; ECTHPEP.
DR	EMBL; D10483; ECAP402.
DR	EMBL; U14003; ECUW93.
DR	PIR; A00671; DEECK.
DR	PIR; S40531; S40531.
DR	ECODGENE; EGI0998; THRA.
DR	PROSITE; PS00324; ASPARTOKINASE.
KM	TRANSFERASE, KINASE, OXIDOREDUCTASE, THREONINE BIOSYNTHESIS; NADP;
KM	ALLOSTERIC ENZYME; MULTIFUNCTIONAL ENZYME.
FT	DOMAIN 1 249 ASPARTOKINASE I.
FT	DOMAIN 250 470 INTERFACE.
FT	DOMAIN 471 820 HOMOSERINE DEHYDROGENASE I.
FT	NP BIND 471 478 NADP (POTENTIAL).
FT	CONFLICT 113 113 Q -> E (IN REF. 4).
FT	CONFLICT 230 230 N -> D (IN REF. 3).

W P S R E H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:20:01 1996; MasPar time 5.44 Seconds
219.061 Million cell updates/sec

Tabular output not generated.

Title: >P60535
Description: (1-144) from p60535.ppe
Perfect Score: 1008
Sequence: 1 mwlgslilgtvacsisapx.....enlkdfllvxpfdwepvqx 144

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 30.234; Variance 133.218; scale 0.227

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description	Pred. No.
1	1008	100.0	144	2	P81886	Sequence of human gra	3.92e-84
2	1008	100.0	144	3	P60535	Colony stimulating fa	3.92e-84
3	1002	99.4	144	13	R71118	GM-CSF encoded by clo	1.48e-83
4	1002	99.4	144	3	P60418	Human granulocyte mac	1.48e-83
5	1002	99.4	144	2	P70657	Sequence of a human g	1.48e-83
6	1002	99.4	144	1	R04098	Metaprotease gen	1.48e-83
7	1002	99.4	144	2	P81885	Sequence of human gra	1.48e-83
8	993	98.5	144	1	P80527	Granulocyte macrophag	1.08e-82
9	993	98.5	144	2	P70656	Sequence of a human g	1.08e-82
10	976	96.8	142	2	P94855	Human granulocyte mac	4.63e-81
11	899	89.2	131	2	P70351	Sequence of granulocy	1.11e-73
12	895	88.8	131	3	P60350	Human granulocyte mac	2.69e-73

13	871	86.4	127	8	R41540	r-h-GM-CSF.	5.33e-71
14	871	86.4	127	3	R13215	Oxidised GM-CSF.	5.33e-71
15	871	86.4	127	7	R33774	Recombinant human Gra	5.33e-71
16	871	86.4	128	1	P90118	Synthetic human granu	5.33e-71
17	871	86.4	128	1	P90115	Synthetic human granu	5.33e-71
18	864	85.7	127	14	R72357	Human granulocyte mac	2.49e-70
19	864	85.7	127	1	P91061	Human granulocyte-mac	2.49e-70
20	864	85.7	127	1	P91890	Amino acid sequence o	2.49e-70
21	862	85.5	128	1	R03199	New human granular ma	3.87e-70
22	861	85.4	128	1	P81001	Sequence (I) of human	4.82e-70
23	860	85.3	127	2	R08268	Crystalline recombinan	6.00e-70
24	857	85.0	127	7	R33775	Human Leu23-GM-CSF mu	1.16e-69
25	857	85.0	132	2	P70363	Sequence of human gra	1.16e-69
26	848	84.1	275	5	R26360	PIXY 344.	8.43e-69
27	848	84.1	275	3	R20114	Human IL-3/GM-CSF fus	8.43e-69
28	848	84.1	275	2	R11067	IL-3/GM-CSF fusion pr	8.43e-69
29	848	84.1	275	4	R23852	IL-3/GM-CSF fusion pr	8.43e-69
30	841	83.4	133	14	R72358	Human granulocyte mac	3.93e-68
31	841	83.4	271	2	R11066	GM-CSF/IL-3 fusion pr	3.93e-68
32	841	83.4	271	4	R23851	GM-CSF/IL-3 fusion pr	3.93e-68
33	841	83.4	271	3	R20113	Human GM-CSF/IL-3 fus	3.93e-68
34	841	83.4	271	5	R26359	PIXY 321.	3.93e-68
35	835	82.8	131	2	P70364	Sequence of human gra	1.47e-67
36	826	81.9	133	3	R13164	hGM-CSF[Leu23Asp27Glu	1.07e-66
37	821	81.4	144	4	R23662	Ovine GM-CSF.	3.20e-66
38	771	76.5	143	2	P94870	Sequence of bovine gr	1.88e-61
39	767	76.1	144	10	R54818	CHEF-2.	4.52e-61
40	752	74.6	144	5	R25699	CaGM-CSF.	1.21e-59
41	418	41.5	118	3	P50294	Sequence of mammalian	3.32e-28
42	416	41.3	118	2	R07611	Murine granulocyte-ma	5.09e-28
43	172	17.1	23	2	R10325	Granulocyte macrophag	3.54e-06
44	153	15.2	27	1	P91151	Wild-type human granu	1.36e-04
45	143	14.2	20	2	P70733	Sequence of leader po	8.96e-04

ALIGNMENTS

RESULT 1
ID P81886 standard; protein; 144 AA.
AC P81886;
DT 29-DEC-1990 (first entry)
DE Sequence of human granulocyte macrophage colony stimulating factor
(GM-CSF)
KW Lymphokine; interleukin-3; cancer therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein 18..144
FT Region 44..46
FT /note="Region R1"
FT Region 54..56
FT /note="Region R2"
PN W08805786-A.
PD 11-AUG-1988.
PF 05-FEB-1988; U00335.
PR 06-FEB-1987; US-011794.
PA (GENE-) Genetics Inst.
PI Clark SC, Wong GG, Donahue RE;
DR WPI; 88-235149/33.
DR N-PSDB; N82363.
PT Colony stimulating factors having reduced carbohydrate levels -
obtd. by replacing and/or deleting asparagine residues in GM-CSF
sequences
PS Disclosure; Table 1, Page 6; 32pp; English.

CC Proteins characterised by possessing GM-CSF-type biological activity
 CC and having specified peptide sequence, except that 1-6 AAs are replaced
 CC and/or deleted within regions Asn-27 - Ser-29 and Asn-37 - Thr-39, such
 CC that one or both of the regions are completely deleted or replaced by a
 CC single AA residue, a dipeptide or a tripeptide sequence other than
 CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
 CC claimed are cDNA encoding proteins. Variants are active CSFs which may
 CC be produced in more homogeneous form and which may possess improved
 CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
 SQ Sequence 144 AA;

Query Match 100.0%; Score 1008; DB 2; Length 144;
 Best Local Similarity 95.8%; Pred. No. 3.92e-84;
 Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwqlslllgtvacsisapsrpsqpwvhnaiqearrrllnlsrdtaaeinvev 60
 |||||
 Qy 1 mwqlslllgtvacsisapsrpsqpwvhnaiqearrrllnlsrdtaaeinvev 60
 |||||

Db 61 semfdlqptcltrlykqglsglklkqpltmashykhcpcptscatqitf 120
 |||||
 Qy 61 semfdlqptcltrlykqglsglklkqpltmashykhcpcptscatqitf 120
 |||||

Db 121 esfkenlkdfllvtpfcdwepvq 143
 |||||
 Qy 121 esfkenlkdfllvxpfcdwepvq 143

RESULT 2

ID P60535 standard; Protein; 144 AA.
 AC P60535;
 DT 30-JUL-1991 (first entry)
 DE Colony stimulating factor (CSF) variant.
 KW Colony stimulating factor.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc difference 20
 FT /label= Ser in gibbon CSF
 FT Misc difference 27
 FT /label= Arg in gibbon CSF
 FT Misc difference 53
 FT /label= Ile in gibbon CSF
 FT Misc difference 60
 FT /label= Val in gibbon CSF
 FT Misc difference 117
 FT /label= Thr in human CSF-Thr
 FT Misc difference 117
 FT /label= Ile in human CSF-Ile
 FT Misc difference 134
 FT /label= Thr in gibbon CSF
 FT Misc difference 143
 FT /label= Gly in gibbon CSF
 PN W08600639-A.
 PD 30-JAN-1986.
 PF 04-JUL-1985; E00326.
 PR 06-JUL-1984; US-628342.
 PR 19-SEP-1984; US-652742.
 PR 19-SEP-1984; US-652471.
 PA (SANO J) SANDOZ AG.
 PI Clark SC, Kaufman RJ, Wong GG, Wang EA.
 DR WPI; 86-042122/06.
 DR N-PSDB; N60457.
 PT Recombinant colony stimulating factor protein - used for treating
 PT infection or granulocytopenia or activating neutrophils in

PT animals.
 PS Disclosure; Fig 1; 91pp; English.
 CC The sequence are human CSF variants (CSF-Ile and CSF-Thr), and
 CC gibbon granulocyte-macrophage CSF. The CSFs are lymphokines used
 CC to treat myelosuppression, especially sympotamatic
 CC granulocytopenia.
 SQ Sequence 144 AA;

Query Match 100.0%; Score 1008; DB 3; Length 144;
 Best Local Similarity 95.8%; Pred. No. 3.92e-84;
 Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwqlslllgtvacsisapsrpsqpwvhnaiqearrrllnlsrdtaaeinvev 60
 |||||
 Qy 1 mwqlslllgtvacsisapsrpsqpwvhnaiqearrrllnlsrdtaaeinvev 60
 |||||

Db 61 semfdlqptcltrlykqglsglklkqpltmashykhcpcptscatqitf 120
 |||||
 Qy 61 semfdlqptcltrlykqglsglklkqpltmashykhcpcptscatqitf 120
 |||||

Db 121 esfkenlkdfllvtpfcdwepvq 143
 |||||
 Qy 121 esfkenlkdfllvxpfcdwepvq 143

RESULT 3

ID R71118 standard; Protein; 144 AA.
 AC R71118;
 DT 12-OCT-1995 (first entry)
 DE GM-CSF encoded by clone pcD-human-GM-CSF cDNA insert.
 KW Human; granulocyte-macrophage colony stimulating factor; GM-CSF;
 KW E.coli; quaternary amino ethyl anion exchange chromatography;
 KW red 120 triazinyl dye-ligand affinity chromatography;
 KW gel filtration column chromatography; stimulation; blood cell.
 OS Homo sapiens.
 PN US5391706-A.
 PD 21-FEB-1995.
 PF 16-JUL-1987; 074410.
 PR 16-JUL-1987; US-074410.
 PR 15-DEC-1989; US-455453.
 PR 14-APR-1992; US-870153.
 PR 21-SEP-1993; US-125356.
 PA (SCHE) SCHERING-PLOUGH CORP.
 PI Kosecki RA, Reichert P, Seelig GF, Trotta PP;
 DR WPI; 95-098169/13.
 DR N-PSDB; Q84865.
 PT Purifying granulocyte-macrophage colony-stimulating factor - by
 PT anion-exchange, dye-ligand affinity, gel filtration and
 PT reversed-phase chromatography
 PS Disclosure; Column 3-4; 5pp; English.
 CC This sequence represents human granulocyte-macrophage colony stimulating
 CC factor (GM-CSF). Heterogeneity of the nucleotide sequence and the
 CC amino acid sequence has been observed and this sequence was deposited
 CC in E.coli as ATCC 39923. The GM-CSF protein was isolated using the
 CC method of the invention. The method comprises killing and disrupting
 CC GM-CSF-expressing bacteria and preparing a GM-CSF containing extract
 CC from the disrupted cells. This extract is subjected to quaternary amino
 CC ethyl (QAE) anion exchange chromatography to separate proteases and
 CC produce protease-free GM-CSF fractions. These fractions are subjected
 CC to red 120 triazinyl dye-ligand affinity chromatography to obtain
 CC GM-CSF containing fractions free of hydrophobic impurities. These
 CC fractions are then subjected to gel filtration column chromatography to
 CC produce GM-CSF containing fractions free of high and low mol. wt.
 CC impurities which are then subjected to reversed-phase column

CC chromatography to produce fractions with a purity of greater than 95%.
CC The obtained GM-CSF may be used in clinical situations where the
CC stimulation of blood cell generation is desirable.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 13; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvevi 60
|||||
Qy 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvev 60
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Db 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
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Qy 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
|||||
Db 121 esfkenlkdfllvfpdcwepvq 143
|||||
Qy 121 esfkenlkdfllvfpdcwepvq 143
|||||

RESULT 4

ID P60418 standard; protein; 144 AA.
AC P60418;
DT 01-JAN-1980 (first entry)
DE Human granulocyte macrophage-colony stimulating factor.
KW Granulocyte; macrophage; colony stimulating factor; chemotherap;
KW Neoplastic disease therapy; Infectious disease therapy; ss.
OS Homo sapiens.
PN M08603225-A.
PD 03-JUN-1986.
PF 18-NOV-1985; U02250.
PR 20-NOV-1984; US-673898.
PA (SCHE) SCHERING BIOTECH CO.
PI Yokota T, Lee FD, Rennick D, Arai K;
DR WPI: 86-155831/24.
DR N-PSDB; N60364.
PT New polypeptide(s) for colony stimulation of granulocytes -
PT useful for enhancing body defences against neoplasms and
PT infectious diseases and to overcome myelo:suppression in
PT chemotherapy
PS Disclosure; Fig. 1; 53pp; English.
CC The protein has GM-CSF activity and is useful in elucidating
CC control mechanisms of mammalian immune responses. It is also
CC useful for administration to enhance natural defences against
CC neoplastic and infectious diseases or as an adjunct in chemotherapy
CC to overcome myelosuppression. GM-CSF is prepared by conventional
CC recombinant DNA techniques. The factor has activity on
CC human neutrophilic granulocytes, macrophages and eosinophils.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 3; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvevi 60
|||||
Qy 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvev 60
|||||
Db 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
|||||
Qy 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
|||||

Db 121 esfkenlkdfllvfpdcwepvq 143
|||||
Qy 121 esfkenlkdfllvfpdcwepvq 143
|||||

RESULT 5
ID P70657 standard; Protein; 144 AA.

AC P70657;
DT 18-APR-1991 (first entry)
DE Sequence of a human granulocyte-macrophage colony stimulating
DE factor (hGM-CSF)-like polypeptide isolated from 5637 cell line.
KW AIDS therapy; leukocyte; leucaemia.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Cleavage-site 17..18
FT /note= "for signal peptide"
PN M08702060-A.
PD 09-APR-1987.
PF 03-OCT-1986; U02106.
PR 03-OCT-1985; US-783414.
PA (BIOI) BIOGEN NV.
PA (DELA) DELAMARTER J.
PI Delamarter J, Ernst JF;
DR WPI: 87-108701/15.
DR N-PSDB; N71002.
PT Human granulocyte-macrophage stimulating factor-like
PT polypeptide(s) - produced from recombinant DNA sequence having 5'
PT terminal alteration
PS Example; Fig 2; 61pp; English.
CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein
CC there is a 5' terminal alteration allowing higher yield than the
CC native DNA sequence. The cpds. may be used to reduce the
CC likelihood of infections in immunologically
CC compromised individuals, such as those suffering from AIDS by
CC increasing their white blood cell count.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvevi 60
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Qy 1 mwlgslilgtvacsisaparspsqpwehnaigearrllnlsrdaaemnetvev 60
|||||
Db 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
|||||
Qy 61 semfdlqptclqtrlelykqglsitklkqpltmashyqhpcptscatqitf 120
|||||
Db 121 esfkenlkdfllvfpdcwepvq 143
|||||
Qy 121 esfkenlkdfllvfpdcwepvq 143
|||||

RESULT 6

ID R04098 standard; protein; 144 AA.
AC R04098;
DT 10-SEP-1990 (first entry)
DE Metapyrocatechase gene product.
KW Metapyrocatechase; GM-CSF; leukopaenia; osteomyelodysplasia;
KW granulocyte macrophage colony stimulating factor; ds.
OS Homo sapiens.
PN J02076596-A.
PD 15-MAR-1990.

PPF 13-SEP-1988; 729468.
 PPR 13-SEP-1988; JP-229468.
 PPA (SAGA) Sagami Chem Res Centre.
 DR WPI; 90-128250/17.
 DR N-PSDB; Q04017.
 PPT Human granulocyte macrophage colony stimulating factor derivs. -
 PPT useful for treating diseases due to leukopenia or
 PPT osteomyelodysplasia.
 PS Disclosure; p; Japanese.
 CCC Human GM-CSF derivs. have polypeptide fragment from N-terminal of
 CCC metapycroatechase, bonded at its C-terminal to the N-terminal of
 CCC GM-CSF. Expression vectors pMGM1 and pMGM3 also contain the tac
 CCC promoter/operator and the SD sequence of metapycroatechase.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 1; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlslllgtvacsisaparspsstqpwvhnaigearrlnlsrdtaacmetvevi 60
|||||
|||||
Qy 1 mwlslllgtvacsisaprxspssqpwehvnaigearrlnlsrdtaaxetvexx 60
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61 semfdldeptclatrlrlykagrgslskllkqpltmashykahcpcptscatqiitf 120
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61 semfdldeptclatrlrlykagrgslskllkqpltmashykahcpcptscatqiitf 120

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Db 121 esfkenkdfllvlpdcwepvq 143
    |||||
Qy 121 esfkenkdfllvxpdcwepvq 143

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7. RESULT

AC	P81885	standard; protein; 144 AA.
AC	P81885	
DT	29-DEC-1990	(first entry)
DE	Sequence of human granulocyte macrophage colony stimulating factor (GM-CSF)	
DE	KW	Lymphokine; interleukin-3; cancer therapy.
OS	Homo sapiens.	
Key	BFH	Location/Qualifiers
FT	Peptide	1..17
FT	Protein	18..144
FT	Region	44..46
FT	/note="Region R1"	
FT	Region	54..56
FT	/note="Region R2"	
FT	W08805786-A.	
PN	PD	11-AUG-1988.
PF	PF	05-FEB-1988; U00335.
PR	PR	06-FEB-1987; U5-011794.
PPA	(GENE-) Genetics Inst.	
PPI	Clark SC, Wong GG, Donahue RE;	
DR	WP1	88-235149/33.
DR	N-PSDB	N80223.
DR	Colony stimulating factors having reduced carbohydrate levels -	
PT	obtd. by replacing and/or deleting asparagine residues in GM-CSF	
PT	sequences	
PS	Disclosure; Table 1, Page 6; 32pp; English.	
CCC	Proteins characterised by possessing GM-CSF-type biological activity	
CCC	having a specified peptide sequence, except that 1-6 AAs are replaced	
CCC	and/or deleted within regions Asn-27 - Ser-29 and Asn-37 - Thr-39,	
CCC	that one or both of the regions are completely deleted or replaced	
CCC	single AA residue, a dipeptide or a tripeptide sequence other than	

CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
CC claimed are cDNA encoding proteins. Variants are active CSFs which may
CC be produced in more homogeneous form and which may possess improved
CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;
Best Local Similarity 95.1%; Pred.No.1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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1 mwllqslllllgtvacsisaparspspstqpwehvnaiqearrllnlsrdaemnetvevi 60
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1 mwllqslllllgtvacsisapxrspspsxpwehvnaiqearrllnlsrdaexnetvevx 60
  |||||

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61 semfdlqeptclqrrlelykqglrgsltklkgptmmashykhcpcptpescatqitf 120
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Db 121 esfkenlkdfllvipfdcepvq 143
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Qv 121 esfkenlkdfllvxpfcdcepvq 143

RESULT 8
ID P80527 standard: protein: 144 AA.

AC	24-OCT-1990 (first entry)
DT	Granulocyte macrophage colony stimulating factor.
DE	Granulocyte macrophage colony stimulating factor.
KW	Granulocyte macrophage colony stimulating factor;
KW	cell line U937; ssDNA.

Key	Location/Qualifiers
FF	Misc-difference 18
FT	/label=Ala
FT	/note='N-terminal residue of mature hGM-CSF'
FT	Misc-difference 97
FT	/label=Ile
FT	/note='differs from residue in hGM-CSF from Mo cells'
FT	EP-281069-A.
PN	PD
PD	07-SEP-1988.
PF	01-MAR-1988; 103067.
PR	02-MAR-1987; JP-048580.
PR	(SUMO) Sumitomo Pharm KK.
PA	Nakayama C, Okamoto M, Yanagi H;
PI	WPI: 88-25166/36.
DR	N-PSDB; N8118.
DR	Human granulocyte-macrophage colony stimulating factor
PT	- produced in human cells transfected with exogenous
PT	DNA encoding the factor.
PS	Disclosure; p; English.
CC	The sequence is that of human granulocyte macrophage
CC	stimulating factor (hGM-CSF) derived from the human cell
CC	line U937. The hGM-CSF is useful for the treatment of
CC	infectious diseases or leukocytopenia which are caused
CC	e.g. irradiation therapy or chemotherapy. See also P
CC	Sequence 144 AA;

Query Match 98.5%; Score 993; DB 1; Length 144;
Best Local Similarity 94.4%; Pred.No. 1.08e-82;
Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Db      1 mwllqslmllgtvacsisaparspspstqpwehvnaiqearrllnlsrdaaemnetvevi 60
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Qy      1 mwllqslmllgtvacsisaparspspsxpwehvnaiqearrllnlsrdaaexnetvevx 60
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Db 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 120
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 120

Db 121 esfkenlkdfllvlpfcdwepvq 143
 Qy 121 esfkenlkdfllvlpfcdwepvq 143

RESULT 9

ID P70656 standard; Protein; 144 AA.
 AC P70656;
 DT 18-APR-1991 (first entry)
 DE Sequence of a human granulocyte-macrophage colony stimulating factor (hGM-CSF)-like polypeptide isolated from U937 cell line.
 DE factor (hGM-CSF)-like polypeptide isolated from U937 cell line.
 KW AIDS therapy; leukocyte; leucaemia.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "for signal peptide"
 FT Misc difference 116
 FT /label= Thr in Mo-cell deriv. cDNA
 PN W08702060-A.
 PD 09-APR-1987.
 PF 03-OCT-1986; U02106.
 PR 03-OCT-1985; US-783414.
 PA (BIOJ) BIOGEN NV.
 PA (DEIA/) DELAMARTER J.
 PI Delamarter J, Ernst JF;
 DR WPI; 87-108701/15.
 DR N-PSDB; N71001.
 PT Human granulocyte-macrophage stimulating factor-like
 PT polypeptide(s) - produced from recombinant DNA sequence having 5'
 PT terminal alteration
 PS Example; Fig 1; 61pp; English.
 CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein
 CC there is a 5' terminal alteration allowing higher yield than the
 CC native DNA sequence. The cpds. may be used to reduce the
 CC likelihood of infections in immunologically
 CC compromised individuals, such as those suffering from AIDS by
 CC increasing their white blood cell count.
 SQ Sequence 144 AA;

Query Match 98.5%; Score 993; DB 2; Length 144;
 Best Local Similarity 94.4%; Pred. No. 1.08e-82;
 Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemnetvevi 60
 Qy 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemnetvev 60
 Db 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 120
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 120

Db 121 esfkenlkdfllvlpfcdwepvq 143
 Qy 121 esfkenlkdfllvlpfcdwepvq 143

RESULT 10

ID P94855 standard; protein; 142 AA.
 AC P94855;

DT 27-JUN-1989 (first entry)
 DE Human granulocyte macrophage colony stimulating factor polypeptide.
 KW Human granulocyte macrophage colony stimulating factor (GM-CSF);
 KW haematopoiesis; depressed blood cells.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 33..464
 FT polyA signal 780..787
 PN EP-299782-A.
 PD 18-JAN-1989.
 PF 15-JUL-1988; 306486.
 PR 17-JUL-1987; US-074988.
 PA (SCHE-) Schering Biotech. Co.
 PI Yokota T, Lee FD, Rennick DM, Arai K-I, Arai N.
 DR WPI; 89-017271/03.
 DR N-PSDB; N93172.
 PT Human granulocyte macrophage colony stimulating factor - used eq for
 PT haematopoiesis stimulation and used in treating depressed blood cell
 PT populations.
 PS Disclosure; fig.1; 40pp; English.

CC Corresponding cDNA sequence is inserted into an expression vector contg.
 CC eg SV40 origin, pref. also a bacterial origin, SV40 early- and SR alpha
 CC promoters, etc. The resulting library is screened and colonies selected
 CC which produce GM-CSF (i.e. those contg. plasmid pcD-human-GM-CSF). Modif-
 CC led forms of GM-CSF are made by producing mutant forms of cDNA esp. using
 CC cassette mutagenesis. These mutants can be glycosylated or non-glycosyl-
 CC ated, substd. (1-2 fold), deleted (1-fold) or inserted (1-fold) forms of
 CC GM-CSF. GM-CSF is useful in the treatment of myeloid hypoplasia and stim-
 CC ulates regeneration of the haematopoietic system following eg bone marrow
 CC transplants and some cancer treatments. Mutant forms show reduced side
 CC effects, improved stability towards proteases and increased yields.
 SQ Sequence 142 AA;

Query Match 96.8%; Score 976; DB 2; Length 142;
 Best Local Similarity 94.4%; Pred. No. 4.63e-81;
 Matches 135; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Db 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemnetvevi 58
 Qy 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemnetvev 60

Db 59 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 118
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetscatqitf 120

Db 119 esfkenlkdfllvlpfcdwepvq 141
 Qy 121 esfkenlkdfllvlpfcdwepvq 143

RESULT 11

ID P70351 standard; Protein; 131 AA.
 AC P70351;
 DT 27-APR-1991 (first entry)
 DE Sequence of granulocyte macrophage colony stimulating factor (GM-CSF) in plasmid pHG23.
 KW Cancer therapy; tumoricide.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 2..13
 FT Protein 14..397
 PN EP-211684-A.
 PD 25-FEB-1987.
 PF 15-AUG-1986; 306304.

CC leukemias and anaemias. GM-CSF of greater purity and in larger CC ants. may be useful in bone marrow transplantation after cancer CC therapy.

SQ	Sequence	131 AA;	Query Match	88.8%;	Score	895;	DB	3;	Length	131;
			Best Local Similarity	93.8%;	Pred. No.	2.69e-73;				
			Matches	122;	Conservative	2;	Mismatches	6;	Indels	0;
							Gaps	0;		

RESULT	13
ID	R41540 standard; protein; 127 AA.
AC	R41540;
DT	16-MAR-1994 (first entry)
DE	r-h-GM-CSF.
DE	Recombinant; human; granulocyte colony stimulating factor;
KW	r-h-GM-CSF; GM-CSF; crystals; polyethylene glycol; PEG; activity;
KW	r-h-GM-CSF; GM-CSF; crystals; polyethylene glycol; PEG; activity;
KW	myelodysplasia syndromes; AIDS; cancer.
OS	Homo sapiens.
PN	EP-561429-A.
PD	22-SEP-1993.
PF	04-JUN-1990; 306042.

(HARDY) SOLGERS CONT.
 TALLMONT G. Le HW, Nagabhushan TL, Reichert P, Trotta PP;
 WP1; 93-296728/38.
 PR Prepn. of crystalline granulocyte-macrophage colony-stimulating
 PR factor - obtd. by equilibrating soln. contg. GM-CSF and
 PR polyethylene glycol, used for treating myelodysplasia syndromes,
 PR AIDS and cancer
 PT
 PS Disclosure; Page 3; 6pp; English.
 CC This sequence represents recombinant human granulocyte macrophage
 CC colony stimulating factor (r-hGM-CSF). Crystals of this protein
 CC were produced using the method of the invention. This method
 CC comprises equilibrating a solution of GM-CSF against a solution that
 CC causes the solution of GM-CSF to become more concentrated and to
 CC form GM-CSF crystals, where the equilibrated solution of GM-CSF
 CC contains polyethylene glycol (PEG) with a molecular weight of 8,000
 CC and 40-250 mg/ml of GM-CSF. The crystalline GM-CSF retains of full
 CC activity so that upon redissolution in an aq. system it possessed the
 CC same activity as the GM-CSF starting material used in preparing the
 CC crystals. The GM-CSF can be used for the treatment of myelodysplasia
 CC syndromes, AIDS and cancer.
 CC Sequence 127 AA;
 SQ

```

Query Match      86.4%; Score 871; DB 8; Length 127;
Best Local Similarity 94.4%; Pred. No. 5.33e-71;
Matches 119; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 aparspsstqpwhevnaigearllnlsrdaaenmetviseimfdlqptclqrle 60
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QV 18 aprspsstqpwhevnaigearllnlsrdaaenmetviseimfdlqptclqrle 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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 W P S R E A
 (TW)

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 Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:19:26 1996; MacPar time 6.88 Seconds
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Tabular output not generated.

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 Perfect Score: 1008
 Sequence: 1 mwqlsllllgtvacsapx.....enlkdfllvpfdewepvqx 144

Scoring table: PAM 150
 Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir46
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
 13:unrev2

Statistics: Mean 41.316; Variance 95.998; scale 0.430

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1002	99.4	144	2	FOHUGM granulocyte-macrophage	3.80e-153
2	828	82.1	144	5	JH0469 granulocyte-macrophage	5.21e-122
3	821	81.4	144	11	A61632 granulocyte-macrophage	9.19e-121
4	773	76.7	143	2	FB06GM granulocyte-macrophage	3.14e-112
5	752	74.6	144	5	A44936 granulocyte-macrophage	1.67e-108
6	546	54.2	141	5	A24644 granulocyte-macrophage	2.53e-72
7	536	53.2	141	5	A24636 granulocyte-macrophage	1.37e-70
8	416	41.3	118	2	FQMSGM granulocyte-macrophage	5.37e-50
9	102	10.1	605	6	S33019 hypothetical protein	2.16e-01
10	102	10.1	605	3	QB8E29 BR1F1 protein - huma	2.16e-01
11	100	9.9	581	4	S50769 alpha-glucosidase ho	3.70e-01
12	97	9.6	146	10	D42402 cell surface glycop	8.21e-01

13	93	9.2	90	8	S49112	hypothetical protein	2.33e+00
14	91	9.0	553	5	A42499	mullerian inhibiting	3.87e+00
15	91	9.0	667	3	VCLJGL	env polypeptide prec	3.87e+00
16	90	8.9	567	2	ACFFAL	nicotinic acetylchol	4.98e+00
17	89	8.8	311	5	A25576	apolipoprotein E pre	6.40e+00
18	89	8.8	311	2	LPRTTE	apolipoprotein E pre	6.40e+00
19	89	8.8	312	5	A26189	apolipoprotein E pre	6.40e+00
20	89	8.8	820	1	DEECK	thrA bifunctional en	6.40e+00
21	88	8.7	133	5	JC2202	secretin - mouse	8.21e+00
22	88	8.7	200	2	UNRTCF	ciliary neurotrophic	8.21e+00
23	87	8.6	514	4	S21125	steroid 17alpha-mono	1.05e+01
24	87	8.6	576	12	S01965	DNA-directed DNA pol	1.05e+01
25	87	8.6	865	9	A53186	fluG protein - Emeri	1.05e+01
26	87	8.6	2201	10	A54774	ATP binding cassette	1.05e+01
27	86	8.5	465	13	S20435	neurokinin-3 recepto	1.34e+01
28	86	8.5	500	10	S46328	intermediate filamen	1.34e+01
29	86	8.5	585	3	W2BE26	gene 26 protein - hu	1.34e+01
30	86	8.5	638	7	C64156	hypothetical protein	1.34e+01
31	86	8.5	815	7	A64048	aspartokinase-homose	1.34e+01
32	85	8.4	76	9	S37191	hypothetical protein	1.71e+01
33	85	8.4	199	2	B38285	interleukin-11 precu	1.71e+01
34	85	8.4	403	10	S41708	cyclin B3 - chicken	1.71e+01
35	85	8.4	417	7	C32185	Frz CD protein - Myx	1.71e+01
36	85	8.4	1403	10	S24548	homoeotic protein pro	1.71e+01
37	85	8.4	1403	10	J01397	pros protein - fruit	1.71e+01
38	85	8.4	1407	10	A41089	neuronal precursor p	1.71e+01
39	85	8.4	1951	5	S18253	laminin chain A - fr	1.71e+01
40	85	8.4	3712	13	S28399	laminin chain A - fr	1.71e+01
41	84	8.3	304	10	S44801	FI0E9.2 protein - Ca	2.17e+01
42	84	8.3	418	10	A53120	intracellular coagul	2.17e+01
43	84	8.3	555	13	S20100	Mullerian inhibiting	2.17e+01
44	84	8.3	2429	2	SJHUA	spectrin alpha chain	2.17e+01
45	83	8.2	311	5	JU0036	apolipoprotein E pre	2.76e+01

ALIGNMENTS

RESULT ENTRY TITLE	FOHUGM	#type complete	granulocyte-macrophage colony-stimulating factor precursor - human
ALTERNATE_NAMES	colony-stimulating factor 2; GM-CSF		
ORGANISM	#formal name Homo sapiens	#common name man	
DATE	04-Dec-1986	#sequence_revision 04-Dec-1986	#text_change 18-Aug-1995
ACCESSIONS	C24636; A25169; A01853; A44175; JC1090		
REFERENCE	A91015		
#authors	Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.		
#journal	EMBO J. (1985) 4:2561-2568		
#title	Structure of the chromosomal gene for granulocyte-macrophage colony stimulating factor: comparison of the mouse and human genes.		
#cross-references	MUID:86030234		
#accession	C24636		
#molecule type	DNA		
#residues	1-144	#label MIY	
#cross-references	EMBL:X03021		
REFERENCE	A25169		
#authors	Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKeerghan, K.; Tushinski, R.J.; Mochizuki, D.Y.; Larsen, A.; Grabstein, K.; Gillis, S.; Cosman, D.		
#journal	Proc. Natl. Acad. Sci. U.S.A. (1985) 82:6250-6254		
#title	Cloning, sequence, and expression of a human granulocyte/macrophage colony-stimulating factor.		


```
#cross-references M01D:85298329
#accession A25169
##molecule_type mRNA
##residues 1-144 ##label CAN
##cross-references GB:M11734
REFERENCE
#authors Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.;
Luh, J.; Arai, K.; Rennick, D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:4360-4364
#title Isolation of cDNA for a human granulocyte-macrophage
colony-stimulating factor by functional expression in
mammalian cells.
#cross-references M01D:85242684
#accession A01853
##molecule_type mRNA
##residues 1-144 ##label LEE
##cross-references GB:M11220
REFERENCE
#authors Wong, G.C.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary,
A.C.; Luxenberg, D.P.; Jones, S.S.; Brown, E.L.; Kay, R.M.;
Orr, E.C.; Shoemaker, C.; Golde, D.W.; Kaufman, R.J.;
Hewick, R.M.; Wang, E.A.; Clark, S.C.
#journal Science (1985) 228:810-815
#title Human GM-CSF: molecular cloning of the complementary DNA and
purification of the natural and recombinant proteins.
#accession A41175
##molecule_type mRNA
##residues 1-116,'T',118-144 ##label WON
##cross-references GB:M10663
##note parts of this sequence, including the amino end of the
mature protein, were confirmed by peptide sequencing
REFERENCE JCI090
#authors Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.
#journal Acta Biochim. Biophys. Sin. (1993) 25:651-655
#title Amplification of human granulocyte-macrophage
colony-stimulating factor cDNA with the method of reverse
transcript-polymerase chain reaction.
#accession JCI090
##status preliminary
##molecule_type protein
##residues 18-21,'C',23-96,'L',98-144 ##label WEN
GENETICS
#gene GDB:CSF2
#map_position 5q23-q31
#introns 53/3; 67/3; 109/3
#description stimulates the differentiation and proliferation of
hematopoietic progenitor cells into granulocytes,
macrophages, and perhaps eosinophils
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
T-cell
FEATURE
1-17 #domain signal sequence #status predicted #label SIG\
18-144 #product granulocyte-macrophage colony-stimulating
factor #status experimental #label MAT\
44,54 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 144 #molecular-weight 16295 #checksum 8567
Query Match 99.4%; Score 1002; DB 2; Length 144;
Best Local Similarity 95.1%; Pred. No. 3.80e-153;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
Db 1 mwlgslllgtvacsisaprspsqpwhehnaigearrllnlsrdaaemnetvev 60
|||||
Qy 1 mwlgslllgtvacsisaprspsqpwhehnaigearrllnlsrdaaemnetvev 60
|||||
Db 61 semfdlqptclqrlelykqglrgsltklkgpltmashykhqcpptscatqitf 120
|||||
Qy 61 semfdlqptclqrlelykqglrgsltklkgpltmashykhqcpptscatqitf 120
|||||
Db 121 esfkenlkdfllvxfdcwepvq 143
|||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
|||||
RESULT 2
ENTRY JH0459 #type complete
TITLE granulocyte-macrophage colony-stimulating factor precursor -
sheep
ALTERNATE_NAMES colony-stimulating factor 2; GM-CSF
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
18-Jun-1993
ACCESSIONS JH0459; S16730
REFERENCE JH0459
#authors McInnes, C.J.; Haig, D.M.
#journal Gene (1991) 105:275-279
#title Cloning and expression of a cDNA encoding ovine
granulocyte-macrophage colony-stimulating factor.
#cross-references M01D:92039044
#accession JH0459
##molecule_type mRNA
##residues 1-144 ##label MCI
##cross-references GB:X53561
COMMENT This protein is a glycoprotein cytokine produced and secreted by
various cell types including activated T-cells and macrophages.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
T-cell
FEATURE
1-17 #domain signal sequence #status predicted #label SIG\
18-144 #product granulocyte-macrophage colony-stimulating
factor #status predicted #label MAT\
44 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 144 #molecular-weight 16318 #checksum 9541
Query Match 82.1%; Score 828; DB 5; Length 144;
Best Local Similarity 77.6%; Pred. No. 5.21e-122;
Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
Db 1 mwlgslllgtvacsisaprspsqpwhehnaigearrllnlsrdaaemnetvev 60
|||||
Qy 1 mwlgslllgtvacsisaprspsqpwhehnaigearrllnlsrdaaemnetvev 60
|||||
Db 61 semfdlqptclqrlelykqglrgsltsltgltmmashykhqcpptscatqitf 120
|||||
Qy 61 semfdlqptclqrlelykqglrgsltklkgpltmashykhqcpptscatqitf 120
|||||
Db 121 esfkenlkdfllvxfdcwepvq 143
|||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
|||||
RESULT 3
```

```
ENTRY      A61632      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor precursor -
ORGANISM    sheep
            #formal name Ovis orientalis aries, Ovis ammon aries
            #common name domestic sheep
DATE        21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change
            28-Jul-1995
ACCESSIONS  A61632
REFERENCE    A61632
            #authors O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
            #journal Immunol. Cell Biol. (1991) 69:51-55
            #title Cloning and sequencing of the cDNA for ovine
            granulocyte-macrophage colony-stimulating factor (GM-CSF).
            #accession A61632
            ##status preliminary; not compared with conceptual translation
            ##molecule_type mRNA
            ##residues 1-144 ##label OAB
FEATURE
1-17        #domain signal sequence #status predicted #label SIG
SUMMARY     #length 144 #molecular-weight 16290 #checksum 8953
Query Match 81.4%; Score 821; DB 11; Length 144;
Best Local Similarity 76.9%; Pred. No. 9,19e-121;
Matches 110; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
Db 1 mwlgllllgtvcsfsaptrpsvtrpwhvdaikealslndstdtaavmdetvkv 60
   |||||:||||| ||||| ||||| :||:||||| || ||||| :|||||
Qy 1 mwlgsllllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvkv 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 semfdseptclqtrlelykqglqgsitlsgtmtmashykhcpcptscatqitf 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptclqtrlelykqglqgsitlsgtmtmashykhcpcptscatqitf 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ksfkenlkdfilvxfdwepqv 143
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfilvxfdwepqv 143
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT      4
ENTRY      F0BOGM      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor precursor -
            bovine
ALTERNATE_NAMES  colony-stimulating factor 2; GM-CSF
ORGANISM      #formal name Bos primigenius taurus #common name cattle
DATE          31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
            27-Jan-1995
ACCESSIONS  J10037
REFERENCE    J10037
            #authors Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall,
            J.M.; Picha, K.S.; Cosman, D.; Tushinski, R.J.; Gillis, S.;
            Baker, P.E.
            #journal Mol. Immunol. (1988) 25:843-850
            #title Bovine GM-CSF: molecular cloning and biological activity of
            the recombinant protein.
            #cross-references MUID:89096971
            #accession J10037
            ##molecule_type mRNA
            ##residues 1-143 ##label MAL
COMMENT      This glycoprotein induces granulocyte, macrophage, and eosinophil
            colony formation.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS      cytokine; glycoprotein; growth factor; macrophage; monomer;
            T-cell
FEATURE
```

```
1-17        #domain signal sequence #status predicted #label SIG
18-143      #product granulocyte-macrophage colony-stimulating
            factor #status predicted #label MAL
44,54       #binding site carbohydrate (Asn) (covalent) #status
            predicted
SUMMARY     #length 143 #molecular-weight 16157 #checksum 5779
Query Match 76.7%; Score 773; DB 2; Length 143;
Best Local Similarity 69.2%; Pred. No. 3.14e-112;
Matches 99; Conservative 20; Mismatches 23; Indels 1; Gaps 1;
Db 1 mwlglllllgtvcsfsaptrpntatrpwhvdaikealsllnhsdtdavmdt-evv 59
   |||||:||||| ||||| ||||| :||:||||| || ||||| ||||| |||||
Qy 1 mwlgsllllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvkv 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 sekfdseptclqtrlelyknglqgsitlsgmtmashykhcpcptscatqitf 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptclqtrlelykqglqgsitlsgmtmashykhcpcptscatqitf 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 knfkedkeflilvxfdwepqv 142
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfilvxfdwepqv 143
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT      5
ENTRY      A44936      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor, GM-CSF -
            dog
ORGANISM      #formal name Canis lupus familiaris #common name dog
DATE          17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
            12-Apr-1995
ACCESSIONS  A44936
REFERENCE    A44936
            #authors Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.;
            Boone, T.; Morris, C.F.; Slichter, S.J.; Storb, R.
            #journal Blood (1991) 78:930-937
            #title Molecular cloning and in vivo evaluation of canine
            granulocyte-macrophage colony-stimulating factor.
            #cross-references MUID:91329842
            #accession A44936
            ##status preliminary
            ##molecule_type mRNA
            ##residues 1-144 ##label NAS
            #cross-references NCBI:49738; NCBI:49739
            #note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
SUMMARY     #length 144 #molecular-weight 16137 #checksum 9761
Query Match 74.6%; Score 752; DB 5; Length 144;
Best Local Similarity 69.7%; Pred. No. 1.67e-108;
Matches 99; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
Db 1 mwlglllflgtvcsisaptrspitvrpshvdaiqealsllnsndvtavmnkavkv 60
   |||||:||||| ||||| ||||| :||:||||| ||||| ||||| ||||| |||||
Qy 1 mwlgsllllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvkv 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 sevfdseptclqtrlelykqglqgsitlsgmtmashykhcpcptscatqitf 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptclqtrlelykqglqgsitlsgmtmashykhcpcptscatqitf 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ksfkenlkdfilvxfdwepqv 142
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfilvxfdwepqv 142
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

RESULT 6
ENTRY A24644 #type complete
TITLE granulocyte-macrophage colony-stimulating factor precursor - mouse

ALTERNATE_NAMES
ORGANISM #formal name Mus musculus #common name house mouse
DATE 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Jun-1993

ACCESSIONS A24644
REFERENCE A24644
#authors Delamarter, J.F.; Mermoud, J.J.; Liang, C.M.; Eliason, J.F.; Thatcher, D.R.
#journal EMBO J. (1985) 4:2575-2581
#cross-references MUID:86030236
#accession A24644
#molecule_type mRNA
##residues 1-141 ##label DEL

CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
SUMMARY #length 141 #molecular-weight 16133 #checksum 4526

Query Match 54.2%; Score 546; DB 5; Length 141;
Best Local Similarity 53.1%; Pred. No. 2.53e-72;
Matches 76; Conservative 20; Mismatches 44; Indels 3; Gaps 1;

Db 1 mwlgmllfigivvyslsaptrspitvtrpkhveakealnld---dmpvthneevv 57
||||:||||| | :||| ||| :||| ||| ||| :||| ||| ||| :||| |||
Qy 1 mwlgmllfigivvyslsaptrspitvtrpkhveakealnld---dmpvthneevv 57
||||:||||| | :||| ||| :||| ||| ||| :||| ||| ||| :||| |||

Db 58 snfsfkkltcvqtrikifegqlrgnftklkgalntasytycypptdetctqvtty 117
| : | : ||| ||| : ||| : ||| ||| : ||| : ||| ||| ||| : ||| : |||
Qy 61 semfdlqptclqtrlelykqglgsktkkqplmtmaashykhqcpptscatqkitf 120
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 118 adfidslktfltdipfeckbpqv 140
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 esfkenlkdfllvxpfdwepqv 143
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
ENTRY A24636 #type complete
TITLE granulocyte-macrophage colony-stimulating factor precursor - mouse

ALTERNATE_NAMES
ORGANISM #formal name Mus musculus #common name house mouse
DATE 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 14-Sep-1994

ACCESSIONS A24636; A24645
REFERENCE A91015
#authors Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
#journal EMBO J. (1985) 4:2561-2568
#title Structure of the chromosomal gene for granulocyte-macrophage colony stimulating factor: comparison of the mouse and human genes.
#cross-references MUID:86030234
#accession A24636
#molecule_type DNA; mRNA
##residues 1-141 ##label M1Y
##note the sequence translated from the mRNA differs from that of the DNA in having 139-Ser

REFERENCE A24645
#authors Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn, A.R.

```

```

#journal EMBO J. (1985) 4:2569-2573
#title The structure and expression of the murine gene encoding granulocyte-macrophage colony stimulating factor: evidence for utilisation of alternative promoters.
#cross-references MUID:86030235
#accession A24645
#molecule_type DNA
##residues 1-141 ##label STA

GENETICS
#introns 50/3; 64/3; 106/3
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
SUMMARY #length 141 #molecular-weight 16090 #checksum 4151

Query Match 53.2%; Score 536; DB 5; Length 141;
Best Local Similarity 52.4%; Pred. No. 1.37e-70;
Matches 75; Conservative 20; Mismatches 45; Indels 3; Gaps 1;

Db 1 mwlgmllfigivvyslsaptrspitvtrpkhveakealnld---dmpvthneevv 57
||||:||||| | :||| ||| :||| ||| ||| :||| ||| ||| :||| |||
Qy 1 mwlgmllfigivvyslsaptrspitvtrpkhveakealnld---dmpvthneevv 57
||||:||||| | :||| ||| :||| ||| ||| :||| ||| ||| :||| |||

Db 58 snfsfkkltcvqtrikifegqlrgnftklkgalntasytycypptdetctqvtty 117
| : | : ||| ||| : ||| : ||| ||| : ||| : ||| ||| ||| : ||| : |||
Qy 61 semfdlqptclqtrlelykqglgsktkkqplmtmaashykhqcpptscatqkitf 120
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 118 adfidslktfltdipfeckbpqv 140
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 esfkenlkdfllvxpfdwepqv 143
| : || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
ENTRY F0MSGM #type complete
TITLE granulocyte-macrophage colony-stimulating factor - mouse
ALTERNATE_NAMES colony-stimulating factor 2; GM-CSF
ORGANISM #formal name Mus musculus #common name house mouse
DATE 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 10-Mar-1994

ACCESSIONS A01854
REFERENCE A01854
#authors Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Graill, D.; Nicola, N.A.; Burgess, A.W.; Dunn, A.R.
#journal Nature (1984) 309:763-767
#title Molecular cloning of cDNA encoding a murine haematopoietic growth regulator, granulocyte-macrophage colony stimulating factor.
#cross-references MUID:84245825
#accession A01854
#molecule_type mRNA
##residues 1-118 ##label G00
##cross-references GB:X05906
COMMENT The mRNA for this protein was isolated from lung tissue.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
FEATURE
60,69 #binding site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 118 #molecular-weight 13544 #checksum 2606

Query Match 41.3%; Score 416; DB 2; Length 118;
Best Local Similarity 50.9%; Pred. No. 5.37e-50;
Matches 59; Conservative 17; Mismatches 37; Indels 3; Gaps 1;

```



```
Db 499 llgltagigtstaligkpi-dlqqgltslqiaadadlralqdsvkledsltsls 555
||| :: | : : : ||| : || : : ||| :: || ::
```

Jun 21 12:09 /home/pandya/mertz_08_466_308/P60535.rpr 13

Oy 42 llnlsrdaexnetvevxsemfdlqep-tclqtrlelykqglqgsitkklqplmma 98

Search completed: Fri Jun 21 12:19:43 1996
Job time : 17 secs.

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